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Sequence 141, App
Sequence 111, App
Sequence 116, App
Sequence 176, App
Sequence 3, AppI
Sequence 9, AppI
Sequence 9, AppI
Sequence 545, App
Sequence 544, App
Sequence 550, App
Sequence 557, App
Sequence 535, App
Sequence 21, AppI
Sequence 1, AppI
Sequence 19, AppI
Sequence 22, AppI
Sequence 5509, App
Sequence 1334, App

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HYPOTHETICAL: NO
 ORIGINAL SOURCE: NO
 ORGANISM: *Lycopersicon esculentum*
 STRAIN: Alisa Craig
 DEVELOPMENTAL STAGE: Ripening
 US-07-598-873-1

Query Match 8.7%; Score 28, 6; DB 1; Length 1080;
 Best Local Similarity 61.3%; Pct. No. 5.2%; Mismatches 0; Indels 0; Gaps 0;
 Matches 46; Conservative 31; 0: Mismatches 29; Indels 0; Gaps 0;

Qy 221 TCTGTACCTACGCTTCACTTCACCTGCCTCTGCCAACACCAAGCT 280
 Db 742 TCTTACTCTCTGCTCATCTGATTCAGTTACCATACACCT 683

Qy 281 GTCATGGACACA 295
 Db 682 GCTTTGATACACA 668

RESULT 13
 US-08-073-425-1/C
 Sequence 1, Application US/08073425
 PATENT NO. 5,659,829
 GENERAL INFORMATION:
 APPLICANT: BIRD, COLIN R
 APPLICANT: BONTELLI, JEREMY M.
 APPLICANT: GRIERSON, DONALD
 APPLICANT: RAY, JOHN A
 APPLICANT: SCHUCH, WOLFGANG W
 TITLE OF INVENTION: PLANTS
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
 STREET: 1100 New York Avenue, N.W.
 CITY: WASHINGTON
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005-1918

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-905/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/073,425
 FILING DATE: 09-JUN-1993
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: DEAN, DONALD B.
 REGISTRATION NUMBER: 23,048
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-851-3000
 TELEFAX: 202-522-0944

TELEFAX: 617-522-0139
 INFORMATION FOR SEQ ID NO: 1:
 SOURCE: KUULI, S PIPAL N
 LENGTH: 31080 base pairs
 TFFER: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULAR TYPE: DNA
 HYPOTHETICAL: NO
 ORIGINAL SOURCE: NO
 ORGANISM: *Lycopersicon esculentum*
 STRAIN: Alisa Craig
 DEVELOPMENTAL STAGE: Ripening
 US-08-073-425-1

Query Match 8.7%; Score 28, 6; DB 1; Length 1080;
 Best Local Similarity 61.3%; Pct. No. 5.2%; Mismatches 0; Indels 0; Gaps 0;
 Matches 46; Conservative 31; 0: Mismatches 29; Indels 0; Gaps 0;

Qy 221 TCTGTACCTACGCTTCACTTCACCTGCCTCTGCCAACACCAAGCT 280
 Db 742 TCTTACTCTCTGCTCATCTGATTCAGTTACCATACACCT 683

Qy 281 GTCATGGACACA 295
 Db 682 GCTTTGATACACA 668

RESULT 14
 US-08-096-531-1/C
 Sequence 1, Application US/08096531
 PATENT NO. 5,741,356
 GENERAL INFORMATION:
 APPLICANT: BIRD, COLIN R
 APPLICANT: GRIERSON, DONALD
 APPLICANT: RAY, JOHN A
 APPLICANT: SCHUCH, WOLFGANG W
 TITLE OF INVENTION: DNA CONSTRUCTS, CELLS AND PLANTS
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
 STREET: Ninth Floor, 1100 New York Avenue, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005-3918
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-905/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/396,531
 FILING DATE: 09-JUN-1993
 CLOSING DATE: 800
 PRIORITY DATA:
 PRIORITY NUMBER: US 07/0847,037
 FILING DATE: 16-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: KUULI, S PIPAL N
 REGISTRATION NUMBER: 16,773
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-851-3000
 TELEFAX: 202-522-0944
 TELEFAX: 617-522-0139
 INFORMATION FOR SEQ ID NO: 1:
 SOURCE: CHARACTERISTICS:
 LENGTH: 31080 base pairs
 TFFER: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULAR TYPE: DNA
 HYPOTHETICAL: NO
 ORIGINAL SOURCE: NO
 ORGANISM: *Lycopersicon esculentum*
 STRAIN: Alisa Craig
 DEVELOPMENTAL STAGE: Ripening
 US-08-396-531-1

Query Match 8.7%; Score 28, 6; DB 1; Length 1080;
 Best Local Similarity 61.3%; Pct. No. 5.2%; Mismatches 0; Indels 0; Gaps 0;
 Matches 46; Conservative 31; 0: Mismatches 29; Indels 0; Gaps 0;

Qy 221 TCTGTACCTACGCTTCACTTCACCTGCCTCTGCCAACACCAAGCT 280
 Db 742 TCTTACTCTCTGCTCATCTGATTCAGTTACCATACACCT 683

Qy	194	CIGGCGCCATCTCCCGAACACATTGATAGATGTCAGCTAACAGGC	253		
Db	183	GGCGGACTCTAACAGACTGACTCTCCCGAACACATTGATAGATGTCAGCTAACAGGC	242		
Db	254	GGCGGACTCTAACAGACTGACTCTCCCGAACACATTGATAGATGTCAGCTAACAGGC	313		
Qy	243	CACTGCATCTCGCTGCCTCACACAGACAGAGGTGTCATGAGACAGAGTG	302		
Db	314	CACTGCATCTCGCTGCCTCACACAGACAGAGGTGTCATGAGACAGAGTG	313		
Db	374	GGATTCGAAAGTATGGCACTG	398		
RESULT 2					
US-10-198-846-1131/c					
Publication 13311; Application US/1019846					
GENERAL INFORMATION:					
Applicant No.: US20030099974A1					
Applicant: Xu, Yongyo					
Applicant: Lillie, James					
Applicant: Wang, Youchen					
Applicant: Steinmann, Kathleen					
Title of Invention: Novel genes, compositions, kits, and methods					
Title of Invention: For identification, assessment, prevention, and					
title of invention: therapy of breast cancer					
File Reference: WRI-049					
Current Application Number: US/10-198, 846					
Current Filing Date: 2002-07-18					
Prior Application Number: 60/306, 220					
Prior Filing Date: 2001-07-18					
Number of SEQ ID Nos.: 1,4084					
Software: FASTQD for Windows Version 4.0					
SEQ ID NO: 11311					
Length: 4543					
Type: DNA					
Organism: Homo sapiens					
Query Match					
Best Local Similarity: 99.4%; Score: 321.8; DB: 14; Length: 4543;					
Matches: 343; Conservative: 0; Mismatches: 2; Indels: 0; Gaps: 0;					
3 GGCAGGAGGATGAGTGGATCCCGAACACAGGGGGGAGAACAGCG	62	Qy	8 CAGCGATGATGTGATACCGGGGACACAGCGACGGCGAGAACGCTTG	67	
Db	2 CAGCGATGATGTGATACCGGGGACACAGCGACGGCGAGAACGCTTG	61	Qy	68 AAGTGGAAAGTGGATGCACTGGCCCTGGCGCGAGATGGGGTGAATCTG	127
1089 GCGCGGAGGGGGATGGTGGATACCGGGGGACACACAGGGGGGGCA	1030	Db	62 AAGTGGAAAGTGGATGCACTGGCCCTGGCGCGAGATGGGGTGAATCTG	121	
63 CTTGGAGTGAAGAAACTGGTGGACTGGCGCTCTGGCTGGATATGGTGTGATA	122	Qy	128 CCACCTGGAGACACATGGTGACTGGCTTGTGATAGAATGAGTACAGTG	187	
Db	1029 CTTGGAGTGAAGAAACTGGTGGACTGGCGCTCTGGCTGGATATGGTGTGATA	970	Db	122 CCACCTGGAGACACATGGTGACTGGCTTGTGATAGAATGAGTACAGTG	181
123 CTGTCGCACTCGGAGGACGACATTTGGTGGCTTCAGAAAGTGGTGGCTAACAGC	182	Qy	188 CTAATCTGGAGTGGCTGGGAGATGGGGTGAATCTG	247	
Db	969 CTGTCGCACTCGGAGGACGACATTTGGTGGCTTCAGAAAGTGGTGGCTAACAGC	910	Db	182 CTAATCTGGAGTGGCTGGGAGATGGGGTGAATCTG	241
183 GTCGGACTCTGGAGAGTGGTGGCTGGGAGCTGGTGGCTGGCTTGTGACT	242	Qy	248 GCACCTGGCTGGCTCAACACAGGGGGTCAATGGACACAGAGATGGGT	307	
Db	905 GTCGGACTCTGGAGAGTGGTGGCTGGGAGCTGGTGGCTGGCTTGTGACT	850	Db	242 GCACCTGGCTGGCTGGCTCAACACAGGGGGTCAATGGACACAGAGATGGGT	301
243 CCACTGCATCTCGCTGGCTGCTAACACAGGGGGTGGCTGGCTGGCTGGCTGG	302	Qy	308 TCCAAAGATGGGCACTG	327	
Db	849 CCACTGCATCTCGCTGGCTGCTAACACAGGGGGTGGCTGGCTGGCTGGCTGG	790	Db	302 TCCAAAGATGGGCACTG	321
Qy	303 GGATTCGAAAGTATGGCACTG	37	RESULT 4		
Db	789 GGATTCGAAAGTATGGCACTG	785	US-10-205-823-382/c		
Sequence 302; Application US/10205823					
Publication No.: US20030108963A1					
GENERAL INFORMATION:					
Applicant: Schleifer, Robert					
Applicant: Monahan, John E.					
Applicant: Endee, Wilson O.					
Applicant: Gannavarapu, Manjula					
Applicant: Gorbsch, Sebilia					
Applicant: Hoerlich, Sebastian					
Applicant: Kamatkar, Shubhangi					
Applicant: Wonsley, Karen M.					
Applicant: Glatt, Karen					
Applicant: Zhao, Xunlei					
Applicant: Anderson, Dustin					
Title of Invention: Methods for identification, assessment, prevention, and					
Title of Invention: therapy of prostate cancer					
File Reference: WRI-044					
Current Application Number: US/10-205, 823					
Prior Application Number: 60/307, 982					
Prior Filing Date: 2001-07-25					
RESULT 3					
US-09-960-352-4677					
Sequence 4677; Application US/09960352					
Patent No.: US2002017139A1					

APPLICANT: Cheung, Andrew K.
 TITLE OF INVENTION: Pseudorabies Virus Deletion Mutants
 TIME OF INVENTION: Involving The EPO and LTR Genes
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS: P. R. Braband
 STREET: 1815 NO. 3352567 University Street
 CITY: Seattle
 STATE: WA
 ZIP/POSTAL: 98103
 COUNTRY: USA

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER TYPE: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Inventor in Release #1.0, Version #1.25
 CURRENT APPLICATION NUMBER: US/07/945, 283
 PRIORITY NUMBER: US/07/945, 283
 FILED DATE: 1992/01/11
 CLASSIFICATION: 44
 ATTORNEY/AGENT INFORMATION:
 NAME: Rindtorp, Curtis P.
 ADDRESS: 1000 University Street, Seattle, WA 98101
 TELEPHONE: (206) 543-4128
 FAX: (206) 543-4128
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8138 base pairs
 NUCLEOTIDE: no
 STRANDEDNESS: double
 TOPOLOGY: Linear
 MOLECULE TYPE: DNA (genomic)
 INFORMATION: NO
 ANTI SENSE: NO
 ORIGINAL SOURCE:
 FOREIGN/SM: Pseudorabies virus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 622..6495
 FEATURE:
 NAME/KEY: variation
 LOCATION: replace(109, "g")
 FEATURE:
 NAME/KEY: variation
 LOCATION: replace(109, "g")
 FEATURE:
 NAME/KEY: variation
 LOCATION: replace(1567, "c")
 FEATURE:
 NAME/KEY: variation
 LOCATION: replace(1581, "c")
 FEATURE:
 NAME/KEY: variation
 LOCATION: replace(1566, "c")
 FEATURE:
 NAME/KEY: variation
 LOCATION: replace(7010, "g")
 ;
 US-07-945-283-1

Alignment Scores:
 Pred. No.: 0.585
 Score: 83.00
 Percent Similarity: 40.40%
 Best Local Similarity: 28.50%
 Query Match: 13.80%
 Db: 3
 Gaps: 4

US-09-541-462B-2 (1-108) x US-09-268-140-11 (1-2339)

Alignment Scores:
 Pred. No.: 0.795
 Score: 90.00
 Percent Similarity: 40.96%
 Best Local Similarity: 31.88%
 Query Match: 14.61%
 Db: 1
 Gaps: 6

US-09-541-462B-2 (1-108) x US-09-945-283-1 (1-8438)

Query 6 AspValAspThrProSerGlyAlaLysLysArgPheLeuValLys 25
 Db 1568 GATTTAGTGGGGGCCGTCGAGCTGGTCCGGGAGGTAGA 1522

Query 26 LysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAlaSpAsnCysAlaIleCys 45

RESULT 5
 US-09-268-140-11
 ; Sequence 11, Application US/09268140
 ; Patent No. 628176
 ; GENERAL INFORMATION:
 ; APPLICANT: Gemmill, Robert M.
 ; TITLE OF INVENTION: TRCB, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED
 ; FILE REFERENCE: 93445-0004
 ; CURRENT APPLICATION NUMBER: US/09/268 140
 ; CURRENT FILING DATE: 2000-03-12
 ; PRIORITY FILING DATE: 1998-03-12
 ; NUMBER OF SEQ ID NOS: 46 2.0
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO: 11
 ; LENGTH: 2339
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-268-140-11

Alignment Scores:
 Pred. No.: 0.585
 Score: 83.00
 Percent Similarity: 40.40%
 Best Local Similarity: 28.50%
 Query Match: 13.80%
 Db: 3
 Gaps: 4

US-09-541-462B-2 (1-108) x US-09-268-140-11 (1-2339)

Alignment Scores:
 Pred. No.: 0.585
 Score: 83.00
 Percent Similarity: 40.40%
 Best Local Similarity: 28.50%
 Query Match: 13.80%
 Db: 3
 Gaps: 4

US-09-541-462B-2 (1-108) x US-09-268-140-11 (1-2339)

Alignment Scores:
 Pred. No.: 0.585
 Score: 83.00
 Percent Similarity: 40.40%
 Best Local Similarity: 28.50%
 Query Match: 13.80%
 Db: 3
 Gaps: 4

US-09-541-462B-2 (1-108) x US-09-268-140-11 (1-2339)

Alignment Scores:
 Pred. No.: 0.585
 Score: 83.00
 Percent Similarity: 40.40%
 Best Local Similarity: 31.88%
 Query Match: 14.61%
 Db: 1
 Gaps: 6

US-09-541-462B-2 (1-108) x US-09-945-283-1 (1-8438)

Query 6 AspValAspThrProSerGlyAlaLysLysArgPheLeuValLys 25
 Db 1568 GATTTAGTGGGGGCCGTCGAGCTGGTCCGGGAGGTAGA 1522

Query 26 LysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAlaSpAsnCysAlaIleCys 45

RESULT 6
 US-09-268-140-1
 ; Sequence 1, Application US/09268140
 ; Patent No. 628176
 ; GENERAL INFORMATION:
 ; APPLICANT: Drabkin, Robert M.

Db 304 CAAGGTTAGGCGCAC 318
 |||:|||||:|||||:
 RESULT 5

US-09-770-791-20
 Sequence 20 Application US-09770791

US-10-205-821-382/C
 Publication No. US20030096581

GENERAL INFORMATION:
 APPLICANT: Schirmer, Robert E.

APPLICANT: Monahan, John E.

APPLICANT: Entwistle, Wilson C.

APPLICANT: Gammon, Julia

APPLICANT: Gordon, Brian

APPLICANT: Hockenberry, Stephen

APPLICANT: Kanaoka, Shobu

APPLICANT: Noyce, Angela M.

APPLICANT: Ghatti, Farah

APPLICANT: Anderson, Dustin

APPLICANT: Tamm, Kristin

APPLICANT: Invention: NOVEL METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

TREATMENT OF INVENTION: THERAPY OF PROSTATE CANCER

FILE REFERENCE: WO-04-0205, 823

CURRENT APPLICATION NUMBER: US-10-205, 823

PRIOR APPLICATION NUMBER: 60/307, 982

PRIOR FILING DATE: 2001-07-25

PRIOR APPLICATION NUMBER: 60/314, 356

PRIOR FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/325, 020

PRIOR FILING DATE: 2001-09-15

PRIOR APPLICATION NUMBER: 60/411, 746

PRIOR FILING DATE: 2001-12-12

PRIOR APPLICATION NUMBER: 60/362, 158

PRIOR FILING DATE: 2002-03-05

NUMBER OF SEQ ID NOs: 455

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 382

LOC NO/H: 311

TYPE: DNA

ORGANISM: Homo sapiens

US-10-205-823-382

Alignment Scores:

Prod. No.: 2-038-65

Score: 554.00

Percent Similarity: 100.00%

Best Local Similarity: 99.94%

Query Match: 14

Length: 5111

Matches: 98

Conservative: 0

Mismatches: 0

Indels: 0

Gap:

0

US-09-541-462B-2 (1-108) × US-10-205-823-382 (1-511)

Length: 5111

Matches: 98

Conservative: 0

Mismatches: 0

Indels: 0

Gap:

0

US-09-541-462B-2

Length: 5111

Matches: 98

Conservative: 0

Mismatches: 0

Indels: 0

Gap:

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US-09-770-791-20

Length: 390

Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

Gap:

2

US-09-770-791-20 (1-390)

Length: 390

Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

Gap:

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US-09-541-462B-2 (1-108) × US-09-770-791-20 (1-390)

Length: 390

Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

Gap:

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US-09-541-462B-2 (1-108)

Length: 390

Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

Gap:

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US-09-541-462B-2

Length: 390

Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

Gap:

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US-09-770-791-20

Length: 390

Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

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US-09-770-791-20

Length: 390

Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

Gap:

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US-09-770-791-20

Length: 390

Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

Gap:

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US-09-770-791-20

Length: 390

Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

Gap:

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US-09-770-791-20

Length: 390

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Conservative: 7

Mismatches: 9

Indels: 11

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US-09-770-791-20

Length: 390

Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

Gap:

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US-09-770-791-20

Length: 390

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Conservative: 7

Mismatches: 9

Indels: 11

Gap:

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US-09-770-791-20

Length: 390

Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

Gap:

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US-09-770-791-20

Length: 390

Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

Gap:

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US-09-770-791-20

Length: 390

Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

Gap:

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US-09-770-791-20

Length: 390

Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

Gap:

2

US-09-770-791-20

Length: 390

Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

Gap:

2

US-09-770-791-20

Length: 390

Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

Gap:

2

US-09-770-791-20

Length: 390

Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

Gap:

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US-09-770-791-20

Length: 390

Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

Gap:

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US-09-770-791-20

Length: 390

Matches: 92

Conservative: 7

Mismatches: 9

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US-09-770-791-20

Length: 390

Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

Gap:

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US-09-770-791-20

Length: 390

Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

Gap:

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US-09-770-791-20

Length: 390

Matches: 92

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Gap:

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US-09-770-791-20

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Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

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US-09-770-791-20

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Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

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US-09-770-791-20

Length: 390

Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

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US-09-770-791-20

Length: 390

Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

Gap:

2

US-09-770-791-20

Length: 390

Matches: 92

Conservative: 7

Mismatches: 9

Indels: 11

Gap:

2

US-09-770-791-20

